

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 10:44:34 ; Search time 2024.2 Seconds  
(without alignments)  
5924.458 Million cell updates/sec

Title: US-09-602-833a-1  
Perfect score: 1116  
Sequence: 1 atggagacataaagtgtgtgtt.....cttttagccttcaatttga 1116

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size : 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:\*  
1: em\_estfun:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estom:\*  
5: em\_estcpl:\*  
6: em\_estcha:\*  
7: em\_estro:\*  
8: em\_estov:\*  
9: em\_hic:\*  
10: gb\_estl:\*  
11: gb\_est2:\*  
12: gb\_hic:\*  
13: gb\_gss:\*  
14: em\_gss\_fun:\*  
15: em\_gss\_hum:\*  
16: em\_gss\_hiv:\*  
17: em\_gss\_pin:\*  
18: em\_gss\_pro:\*  
19: em\_gss\_rtd:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	138	12.4	370	11	BG197958 RS17210
2	138	12.4	377	11	BG203142 RST22516
3	137	12.3	598	13	AO670712 HS_5449_A
4	126	11.3	408	11	BG210970 RST30524
5	125	11.2	470	10	AL120256 DKFZP761J
6	125	11.2	669	10	AL133928 DKFZP761J
7	72	6.5	370	10	AV690138 AV690138
8	64	5.7	377	10	AI399758 TG63a12.x
9	46	4.1	298	11	BF840611 MRI-HT106
10	41	3.7	453	13	AO791237 HS_5495_A
11	41	3.7	560	13	AO427288 CITBI-EI-
12	41	3.7	562	13	AO488137 RPT-11-2

c	13	41	3.7	572	13	AO427239 CITBI-EI-
c	14	38	3.4	483	10	AA422330 vF45B09.r
c	15	38	3.4	526	10	AA416235 vF38B07.r
c	16	38	3.4	1450	12	AK010252 Mos_muscu
c	17	34	3.0	377	11	BF839187 MRI-HT106
c	18	29	2.6	319	10	AI561877 vJ48d03.x
c	19	27	2.6	589	13	AZ412330 1M0185C13
c	20	27	2.4	432	10	AM488294 UT-M-BH3-
c	21	27	2.4	443	10	AA500912 v903d04.r
c	22	27	2.4	462	13	AO729142 HS_5467_B
c	23	22	2.0	561	10	BE369391 601220784
c	24	22	2.0	612	13	AO139351 HS_3082_A
c	25	22	2.0	872	13	AZ550245 ENTES31TR
c	26	21	1.9	346	13	AZ242623 RPT-23-6
c	27	21	1.9	422	10	AA432896 v89c04.r
c	28	21	1.9	521	13	AO703005 HS_5443_B
c	29	21	1.9	536	11	BG360776 947041F12
c	30	21	1.9	546	10	AV835588 AV835588
c	31	21	1.9	557	10	BE110536 UT-R-BJ1-
c	32	21	1.9	587	10	AM399889 707052F02
c	33	21	1.9	605	10	AM400149 707052F02
c	34	21	1.9	663	13	AO975840 RPT-23-3
c	35	20	1.8	238	10	BB001850 BB001850
c	36	20	1.8	293	10	AV074179 AV074179
c	37	20	1.8	303	10	AV168643 AV168643
c	38	20	1.8	422	13	CNS005J3
c	39	20	1.8	450	13	AZ377230 1M0131P21
c	40	20	1.8	624	10	AV537620 AV537620
c	41	20	1.8	735	13	BH022447 GH-MB000
c	42	20	1.8	794	13	B01387 CSRL-130h5-
c	43	20	1.8	854	11	BG917965 602820894
c	44	19	1.7	147	10	BE173953 CM0-HT056
c	45	19	1.7	171	10	AV311842 AV311842

#### ALIGNMENTS

RESULT	1	BG197958	370 bp	MRNA	EST	21-APR-2001
LOCUS		RST17210	Athersys RAGE Library	Homo sapiens	CDNA, mRNA sequence.	
DEFINITION		BG197958				
ACCESSION		BG197958.1	GI:13719645			
VERSION						
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS		Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Dahl,T., Thornton,M., Ramchandran,R., Whittington,J., Lerner,L., Krasnoc,D., McEligott,K., Clark,S., Mays,R., Smith,E., Veloso,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.				
TITLE		Creation of Genome-wide Protein Expression Libraries using Random				
JOURNAL		Nat. Biotechnol. 19 (5), 440 (2001) In press				
COMMENT		Contact: Scott J. Cain				
		Athersys, Inc.				
		3201 Carnegie Ave, Cleveland, OH 44115, USA				
		Tel: 216 431 9800				
		Fax: 216 361 9596				
		Email: scain@athersys.com				
		High quality sequence stop: 324.				
FEATURES		Location/Qualifiers				
source		1..370				
		/organism="Homo sapiens"				
		/db_xref="taxon:9606"				
		/clone_lib="Athersys RAGE Library"				
		/cell_line="HT1080"				
		/note="See 'Creation of Genome-wide Protein Expression				
		Libraries using Random Activation of Gene Expression',				

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT

137 a 65 c 63 g 104 t 1 others

Query Match 12.4%; Score 138; DB 11; Length 370;  
Best Local Similarity 100.0%; Pred. No. 9e-60;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 979 ggcacatgaataatggaagtgacggatgcacacatttgataagaagtatgaaa 1038  
|||||  
Db 48 GGCATGTAATATGGAAGTGAACGGATGCCAACATTTGATTAAGATTAAGAA 107  
|||||  
QY 1039 gccatattgaagccttaagaagaagatctgtccacacttacacaaagtgtct 1098  
|||||  
Db 108 GCCATATTGAAGACCTTAAGAAAGAGATCTGTCCACACTATACCAAGATGTCT 167  
|||||  
QY 1099 tttagcttcaacttga 1116  
|||||  
Db 168 TTTAGCCTTCAACTTTGA 185  
|||||

RESULT 2  
BG203142 377 bp mRNA EST 21-APR-2001  
LOCUS RST22516 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.  
DEFINITION BG203142  
ACCESSION BG203142 GI:13724829  
VERSION BG203142.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE

1 (bases 1 to 377)  
Harrington, J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J.,  
Lerner, L., Krashinsky, D., McElligott, K., Clark, S., Mays, R., Smith, E.,  
Velooso, N., Hess, J., Cochren, K., Lo, K., Offenbacher, J., Danzig, J.  
and Ducar, M.

TITLE

Creation of Genome-wide Protein Expression Libraries using Random

JOURNAL

Activation of Gene Expression  
Nat. Biotechnol. 19 (5), 440 (2001) In press  
Contact: Scott J. Cain

COMMENT  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scain@atersys.com

FEATURES

High quality sequence stop: 377.  
Location/Qualifiers  
1..377  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="Athersys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

BASE COUNT

139 a 66 c 65 g 104 t 3 others

Query Match 12.4%; Score 138; DB 11; Length 377;  
Best Local Similarity 100.0%; Pred. No. 9e-60;  
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 979 ggcacatgaataatggaagtgacggatgcacacatttgataagaagtatgaaa 1038

|||||  
Db 54 GGCATGTAATATGGAAGTGAACGGATGCCAACATTTGATTAAGATTAAGAA 113  
|||||  
QY 1039 gccatattgaagccttaagaagaagatctgtccacacttacacaaagtgtct 1098  
|||||  
Db 114 GCCATATTGAAGACCTTAAGAAAGAGATCTGTCCACACTATACCAAGATGTCT 173  
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QY 1099 tttagcttcaacttga 1116  
|||||  
Db 174 TTTAGCCTTCAACTTTGA 191  
|||||

RESULT 3  
A0670712 598 bp DNA GSS 24-JUN-1999  
LOCUS HS\_5449\_A2 E11.T7A RPCI-11 Human Male BAC Library Homo sapiens  
DEFINITION genomic clone Plate=1025 Col=22 Row=I, DNA sequence.  
ACCESSION A0670712  
VERSION A0670712.1 GI:5203458  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE  
1 (bases 1 to 598)  
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D., and  
Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)  
99380589  
CONTACT: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
or from Research Genetics (info@resgen.com). BAC end Web Server:  
http://www.hpsc.washington.edu  
Plate: 1025 row: I column: 22  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 598.  
Location/Qualifiers  
1..598  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=1025 Col=22 Row=I"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/sex="male"  
/note="Vector: pBAC3.6, Site 1: EcoRI, Site 2: EcoRI.  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRII. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"

FEATURES

High quality sequence stop: 598.  
Location/Qualifiers  
1..598  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="Plate=1025 Col=22 Row=I"  
/clone\_lib="RPCI-11 Human Male BAC Library"  
/sex="male"  
/note="Vector: pBAC3.6, Site 1: EcoRI, Site 2: EcoRI.  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRII. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"

BASE COUNT

185 a 97 c 121 g 187 t 8 others

Query Match 12.3%; Score 137; DB 13; Length 598;  
Best Local Similarity 100.0%; Pred. No. 3.1e-59;  
Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 930 attgtgaagccttattggaacatccatattgataatgccaatgtgaagatggaat 989  
|||||  
Db 183 ATTGTGAAGCCTTATTGGAACATCTCTATTGATTAATGCCAATGTGAAGTGAAT 242  
|||||

QY 990 aatggaagtgaacggagatcgcaacatttgataaagaagtattgaagccttatgta 1049  
|||||  
Db 243 AATGGAAGTGAACGGGATCGCCAACTTTGATTAAGAACTATGAAGCCTATATGGA 302  
QY 1050 agacctaagaagaag 1066  
|||||  
Db 303 AGACCTTAAGAAAGAG 319

RESULT 4  
BG210970 508 bp mRNA EST 21-APR-2001  
LOCUS RST30524 Altherys RAGE Library Homo sapiens cDNA, mRNA sequence.  
DEFINITION BG210970  
VERSION BG210970.1 GI:13732657  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE Harrington J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
Cain, S., Dahl, T., Thornton, M., Ramachandran, R., Whittington, J.,  
Vernier, L., Krasnoc, D., McElligott, K., Clark, S., Mays, R., Smith, E.,  
Velooso, N., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J.,  
and Ducar, M.  
Creation of Genome-wide Protein Expression Libraries using Random  
Activation of Gene Expression  
Nat. Biotechnol. 19 (5), 440 (2001) In press  
CONTACT: Scott J. Cain  
Altherys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scaithersys.com  
High quality sequence stop: 508.  
Location/Qualifiers  
1. 508  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="Altherys RAGE Library"  
/cell\_line="HT1080"  
/note="See 'Creation of Genome-wide Protein Expression  
Libraries using Random Activation of Gene Expression',  
Nature Biotechnology, in press. Note that even though the  
cell type indicated is HT1080, since a random activation  
method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."  
BASE COUNT 182 a 81 c 83 g 160 t 2 others

Query Match 11.3%; Score 126; DB 11; Length 508;  
Best Local Similarity 100.0%; Pred. No. 1.3e-53;  
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 991 atggaagtgaacggagatcgcaacatttgataaagaagtattgaagccttatgta 1050  
|||||  
Db 65 ATGGAAGTGAACGGGATCGCCAACTTTGATTAAGAACTATGAAGCCTATATGGA 124  
QY 1051 gacctaagaagaagaatctgtccagctataccaccaagaagtccttttagccttca 1110  
|||||  
Db 125 GACCTTAAGAAAGAGATGTTCCAGCTATACCAAGAGTGCTTTTAAAGCCTTCAA 184

QY 1111 ctctga 1116  
|||||  
Db 185 CTTTGA 190

RESULT 5  
AL120256 470 bp mRNA EST 25-FEB-2000  
LOCUS DKFZp61J017\_r1 761 (synonym: hamy2) Homo sapiens cDNA clone  
DEFINITION

ACCESSION DKFZp61J017 5', mRNA sequence.  
VERSION AL120256  
AL120256.1 GI:5926155  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE Koehler, K., Beyer, A., Mewes, H.W., Gassenhuber, J., and Wiemann, S.  
EST (Koehler, et al.)  
Unpublished (1999)  
CONTACT: Koehler K  
MIPS  
Am Klopferplatz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Charite,  
Berlin/Germany) within the cDNA sequencing consortium of the German  
Genome Project.  
No sl sequence available.  
This clone (DKFZp61J017) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Location/Qualifiers  
1. 470  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp61J017"  
/clone\_id="761 (synonym: hamy2)"  
/tissue\_type="amygdala"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI"  
BASE COUNT 166 a 73 c 77 g 150 t 4 others

Query Match 11.2%; Score 125; DB 10; Length 470;  
Best Local Similarity 100.0%; Pred. No. 4.4e-53;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 992 tgggaagtgaacggagatcgcaacatttgataaagaagtattgaagccttatgta 1051  
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Db 1 TGGGAAGTGAACGGGATCGCCAACTTTGATTAAGAACTATGAAGCCTATATGGAAG 60  
QY 1052 accttaagaagaagaatctgtccagctataccaccaagaagtccttttagccttca 1111  
|||||  
Db 61 ACCTTAAGAAAGAGATGTTCCAGCTATACCAAGAGTGCTTTTAAAGCCTTCAA 120

QY 1112 ttctga 1116  
|||||  
Db 121 TTTGA 125

RESULT 6  
AL133928 669 bp mRNA EST 25-FEB-2000  
LOCUS DKFZp61O1814\_r1 761 (synonym: hamy2) Homo sapiens cDNA clone  
DEFINITION DKFZp61O1814 5', mRNA sequence.  
ACCESSION AL133928  
VERSION AL133928.1 GI:6602115  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE Ansoorge, W., Winkner, U., Mewes, H.W., Weill, B., and Wiemann, S.  
EST (Ansoorge, W., Winkner, U., Mewes, H.W., Weill, B., and Wiemann, S.)  
Unpublished (1999)  
CONTACT: Ansoorge W

MIPS  
Am Klopferpitz 18a D-82152 Martinsried, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ): Email s.wiemann@dkfz-heidelberg.de;  
sequenced by EMBL (European Molecular Biology Laboratories,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No 5' sequence available.  
This clone (DKFZp76101814) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heuberweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

## FEATURES

Location/Qualifiers

1..669  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="DKFZp76101814"  
/clone\_id="761 (synonym: hamy2)"  
/tissue\_type="amygdala"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"

## BASE COUNT

214 a 118 c 141 g 196 t

## ORIGIN

Query Match 11.2%; Score 125; DB 10; Length 669;  
Best Local Similarity 100.0%; Pred. No. 4.5e-53;  
Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 992 tggaaagcgaacggatgcacacatttgataaagaagtatgaagcctattgag 1051  
|||||  
Db 1 TGGAAAGTGAACGGATGCCACATTTGTATGAAGAGTATGAAGCCCTATATGAAG 60

Qy 1052 accataaagaagaatctgtccacagctacacacaaagtgccttcacac 1111  
|||||  
Db 61 ACCTTAAGAAGAAATCTGTCCACCTATACCAACAAAGTGTCTTACCCCTCAAC 120

Qy 1112 ttgtga 1116  
|||||  
Db 121 TTTGA 125

RESULT 7  
AV690138 370 bp mRNA EST 25-SEP-2000  
LOCUS AV690138 GKC Homo sapiens cDNA clone GKCDNE11 5', mRNA sequence.  
DEFINITION AV690138  
VERSION AV690138.1 GI:10292001  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

## AUTHORS

1 (bases 1 to 370)  
Wu, T., Qian, B., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,  
Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L.,  
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang,  
Y., Gu, Y., Chen, Z., and Han, Z.  
Homo sapiens cDNA GK- clones  
Unpublished (2000)  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801918(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

## FEATURES

Location/Qualifiers

1..370  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"

/clone="GKCDNE11"  
/clone\_id="GKC"  
/tissue\_type="hepatocellular carcinoma"  
/dev\_stage="Adult"  
/lab\_host="SOLR"  
/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2:  
XhoI"

## BASE COUNT

85 a 96 c 113 g 76 t

## ORIGIN

Query Match 6.5%; Score 72; DB 10; Length 370;  
Best Local Similarity 100.0%; Pred. No. 7.3e-26;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 gaactcgtcgaagaacacacaaagcttgcgaagaagaagtggaagccttgaag 111  
|||||  
Db 293 GAACCTGCTGCAGAACACCAAGCTTGCAGGAAGAGAGGTGGAAGCCTTGAGAG 352

Qy 112 agcgcttgag 123  
|||||  
Db 353 AGCGCCTTGAG 364

RESULT 8  
AI399758/c 377 bp mRNA EST 30-MAR-1999  
LOCUS t963a12.x1 Soares\_NHMPU\_S1 Homo sapiens cDNA clone IMAGE:2113438  
DEFINITION 3', mRNA sequence.  
ACCESSION AI399758  
VERSION AI399758.1 GI:4242845  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 377)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert Length: 675 Std Error: 0.00  
Seq primer: -40UP from GABCO  
High quality sequence stop: 363.

Location/Qualifiers

## FEATURES

1..377  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2113438"  
/clone\_id="Soares\_NHMPU\_S1"  
/tissue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pRT73D-Pac  
(Pharmacia) with a modified polylinker; Site\_1: Not I;  
Site\_2: Eco RI. Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NbHM, pregnant uterus  
NbHPU, and fetal heart NbH19M) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of T.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

## REFERENCE

## AUTHORS

1 (bases 1 to 377)  
Wu, T., Qian, B., Huang, Q., Huang, C., Kang, B., Gao, X., Xu, Z., Xiao, H.,  
Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z., Zeng, L.,  
Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Yang,  
Y., Gu, Y., Chen, Z., and Han, Z.  
Homo sapiens cDNA GK- clones  
Unpublished (2000)  
Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801918(ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn

This clone is available at CHGC in Shanghai.

## BASE COUNT

129 a 55 c 63 g 130 t

## ORIGIN

Query Match 5.7%; Score 64; DB 10; Length 377;

Best Local Similarity 100.0%; Pred. No. 9.4e-22;  
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1053 ccttaagaagaatctgttcccgatataccaccagaagtctttgaccttaact 1112

Db 377 CCTTAAGAAAGAAATGCTTCCAGCATACACCAAGTGTCTTTAGCCTCAACT 318

OY 1113 ttga 1116

Db 317 TTGA 314

# RESULT 9

LOCUS BF840611 298 bp mRNA EST 13-JAN-2001

DEFINITION MRL-HT1068-011200-006-a06 HT1068 Homo sapiens cDNA, mRNA sequence.

ACCESSION BF840611 GI:12193121

VERSION BF840611.1

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 298)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,

Nagai, M. A., da Silva, W. J., Zago, M. A., Bordin, S., Costa, F. F.,

Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,

Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare

, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and

Simpson, A. J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

CONTACT: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=MRL&lc2=MRL-HT1068-

011200-006-a06&lc3=2000-12-01&lc4=1)

Seq primer: puc 18 forward

High quality sequence start: 20

High quality sequence stop: 298.

Location/Qualifiers

1. 298

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_11b="HT1068"

/dev\_stage="Adult"

/note="Organ: head,neck; Vector: puc18; Site\_1: SmaI;

Site\_2: SmaI; A mini-library was made by cloning products

derived from ORESFES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the puc 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."

BASE COUNT 94 a 59 c 51 g 94 t

ORIGIN

Query Match 4.1%; Score 46; DB 11; Length 298;

Best Local Similarity 100.0%; Pred. No. 1.6e-12;

Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 794 ttctctgtataaacaagtgactactcttccatcctcatcgcgt 839

Db 241 TTCTCTTGATATAAACAAGTGTGACTTCCCTATTCACGCT 286

# RESULT 10

LOCUS AO791237/c

DEFINITION AO791237 453 bp DNA GSS 03-AUG-1999

ACCESSION HS\_5495\_A2.F06.T7A RPI-11 Human Male BAC library Homo sapiens

VERSION AO791237 genomic clone Plate=1071 Col=12 Row=K, DNA sequence.

KEYWORDS AO791237.1 GI:5698784

SOURCE GSS.

ORGANISM human.

REFERENCE Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

1 (bases 1 to 453)

Mahairas, G. G., Wallace, J. C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M. D. and

Hood, L.

Sequence-tagged connectors: A sequence approach to mapping and

scanning the human genome

Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

99380589

CONTACT: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

401 Queen Anne Avenue North, Seattle, WA 98109, USA

Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Clones are derived from the human BAC library RPI-11. For BAC

library availability, please contact Pieter de Jong

(pieterdejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)

or from Research Genetics (info@resgen.com). BAC end web Server:

http://www.htsc.washington.edu

Seq primer: T7

Plate: 1071 Row: K Column: 12

Class: BAC ends

High quality sequence stop: 453.

Location/Qualifiers

1. 453

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_11b="Plate=1071 Col=12 Row=K"

/sex="male"

/note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI;

Male blood DNA was isolated from one randomly chosen donor

and partially digested with a combination of EcoRI and

EcoRI Methylase. Size selected DNA was cloned into the

pBAC3.6 vector at EcoRI sites"

BASE COUNT 116 a 108 c 78 g 146 t 5 others

ORIGIN

Query Match 3.7%; Score 41; DB 13; Length 453;

Best Local Similarity 100.0%; Pred. No. 6.3e-10;

Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 248 ctctcacaagcagagttcaccttcccaagcagagcgaac 288

Db 383 CTCTCACAAGCAGAGTTCCTCCCAAGCAGAGCANA 343

RESULT 11

LOCUS AQ427288/c

DEFINITION AQ427288 560 bp DNA GSS 24-MAR-1999

ACCESSION CITBI-EI-2568D1.TR CITBI-EI Homo sapiens genomic clone 2568D1, DNA

sequence.

VERSION AQ427288

KEYWORDS AQ427288.1 GI:4500038

SOURCE GSS.

human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 560)  
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.  
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSS: CITBI-EI-2568D1.TF  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetlgr.org  
Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
[http://www.tlgr.org/tldb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html).  
Seq primer: M13 Reverse  
Class: BAC ends.  
Location/Qualifiers  
1..560  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="2568D1"  
/clone\_lib="CITBI-EI"  
/sex="male"  
/cell\_type="sperm"  
/note="Vector: pBelOBAC11; Site\_1: EcoRI; Site\_2: EcoRI; Caltech Human BAC library D"  
BASE COUNT 132 a 134 c 101 g 173 t  
ORIGIN

Query Match 3.7%; Score 41; DB 13; Length 560;  
Best Local Similarity 100.0%; Pred. No. 6.4e-10;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 ctctcacaaggcagagttcacttcccaaggacagagcaaa 288  
|||||  
Db 355 CTCTCACAAGCAGAGTTCCTCCCAAGCAGAGCGCAA 315

RESULT 12 562 bp DNA GSS 24-APR-1999  
AQ488137/c  
LOCUS RPCI-11-264L9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-264L9,  
DEFINITION DNA sequence.  
ACCESSION AQ488137  
VERSION AQ488137.1 GI:4674011  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 562)  
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.  
TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSS: RPCI-11-264L9.TV  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetlgr.org  
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong

(pieter@tlgr.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (<http://inforesgen.com>). BAC end search page:  
[http://www.tlgr.org/tldb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html).  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers  
1..562  
/organism="Homo sapiens"  
/db\_xref="GDB:7601264"  
/db\_xref="taxon:9606"  
/clone="RPCI-11-264L9"  
/clone\_lib="RPCI-11"  
/sex="male"  
/cell\_type="Lymphocytes"  
/note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI; RPCI11 Human Male BAC library"  
BASE COUNT 122 a 152 c 119 g 169 t  
ORIGIN

Query Match 3.7%; Score 41; DB 13; Length 562;  
Best Local Similarity 100.0%; Pred. No. 6.4e-10;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 248 ctctcacaaggcagagttcacttcccaaggacagagcaaa 288  
|||||  
Db 195 CTCTCACAAGCAGAGTTCCTCCCAAGCAGAGCGCAA 155

RESULT 13 572 bp DNA GSS 24-MAR-1999  
AQ427239/c  
LOCUS CITBI-EI-2568B9.TR CITBI-EI Homo sapiens genomic clone 2568B9, DNA  
DEFINITION sequence.  
ACCESSION AQ427239  
VERSION AQ427239.1 GI:4499942  
KEYWORDS GSS.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 572)  
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.  
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other\_GSSS: CITBI-EI-2568B9.TF  
Contact: Shaying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetlgr.org  
Clones are available from Research Genetics (info@resgen.com). BAC end search page:  
[http://www.tlgr.org/tldb/humgen/bac\\_end\\_search/bac\\_end\\_search.html](http://www.tlgr.org/tldb/humgen/bac_end_search/bac_end_search.html).  
Seq primer: M13 Reverse  
Class: BAC ends.  
Location/Qualifiers  
1..572  
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/db\_xref="taxon:9606"  
/clone="2568B9"  
/clone\_lib="CITBI-EI"  
/sex="male"  
/cell\_type="sperm"  
/note="Vector: pBelOBAC11; Site\_1: EcoRI; Site\_2: EcoRI; Caltech Human BAC library D"  
BASE COUNT 134 a 157 c 104 g 177 t  
ORIGIN

Query Match 3.7%; Score 41; DB 13; Length 572;  
 Best Local Similarity 100.0%; Pred. No. 6.4e-10;  
 Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 248 ctctcaagaagcagagctcctcccaagacagagcaaa 288  
 Db 355 CTCCTCAAGGAGAGTTCCTCCCAAGGAGGCAAA 315

# RESULT 14

AA422330 483 bp mRNA EST 16-OCT-1997  
 LOCUS v45b09.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:846713  
 DEFINITION 5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER

FLIGHTLESS-1 GENE PRODUCT ;, mRNA sequence.

ACCESSION AA422330.1 GI:2101146

# VERSION KEYWORDS SOURCE ORGANISM

EST.  
 house mouse.  
 Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 483)

# REFERENCE

## AUTHORS

Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

The WashU-HMI Mouse EST Project

# TITLE

## JOURNAL

## COMMENT

Unpublished (1996)  
 Contact: Maria M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:498865  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 479.  
 Location/Qualifiers

# FEATURES

## source

1. 483  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:846713"  
 /clone\_lib="Soares mouse NbMH"  
 /sex="male"  
 /tissue\_type="heart"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; site 1: Not I; site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TGTTCACATCTGACGTGAGGCGCGGCAAGTTTCTTTTCTTTTCTTTTCTTTT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not  
 I and Eco RI sites of the modified p773 vector. RNA  
 provided by Dr. Minoru Ko, Wayne State Univ. Library  
 constructed and normalized by Bento Soares and M.Fatima  
 Bonaldo."

BASE COUNT 125 a 115 c 120 g 123 t  
 ORIGIN

Query Match 3.4%; Score 38; DB 10; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 cccttgaattaagtaattgaagaagctacattgt 656  
 Db 99 CCCTTGATTAAGTAATTGACCAAGTTCATTGT 136

# RESULT 15

AA416235 526 bp mRNA EST 16-OCT-1997  
 LOCUS v43b07.r1 Soares mouse NbMH Mus musculus cDNA clone IMAGE:846037  
 DEFINITION 5' similar to TR:G440177 G440177 HOMOLOG OF D. MELANOGASTER

FLIGHTLESS-1 GENE PRODUCT ;, mRNA sequence.

ACCESSION AA416235.1 GI:2076503

# VERSION KEYWORDS SOURCE ORGANISM

EST.  
 house mouse.  
 Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 526)

# REFERENCE

## AUTHORS

Marr, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,  
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
 Waterston, R.

The WashU-HMI Mouse EST Project

# TITLE

## JOURNAL

## COMMENT

Unpublished (1996)  
 Contact: Maria M/Mouse EST Project  
 WashU-HMI Mouse EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 MGI:498189  
 Seq primer: -28ml3 rev2 ET from Amersham  
 High quality sequence stop: 482.  
 Location/Qualifiers

# FEATURES

## source

1. 526  
 /organism="Mus musculus"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone\_image="IMAGE:846037"  
 /clone\_lib="Soares mouse NbMH"  
 /sex="male"  
 /tissue\_type="heart"  
 /dev\_stage="4 weeks"  
 /lab\_host="DH10B"  
 /note="Vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; site 1: Not I; site 2: Eco RI; 1st strand cDNA  
 was primed with a Not I - oligo(dT) primer [5',  
 TGTTCACATCTGACGTGAGGCGCGGCAAGTTTCTTTTCTTTTCTTTTCTTTT  
 3']; double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not  
 I and Eco RI sites of the modified p773 vector. RNA  
 provided by Dr. Minoru Ko, Wayne State Univ. Library  
 constructed and normalized by Bento Soares and M.Fatima  
 Bonaldo."

BASE COUNT 140 a 122 c 130 g 134 t  
 ORIGIN

Query Match 3.4%; Score 38; DB 10; Length 526;  
 Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
 Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 619 cccttgaattaagtaattgaagaagctacattgt 656  
 Db 100 CCCTTGATTAAGTAATTGACCAAGTTCATTGT 137

Tue Feb 26 15:53:33 2002

us-09-602-833a-1.rst

Page 8

Search completed: February 26, 2002, 12:31:02  
Job time: 6388 sec

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